

OIPE

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/757,982A

DATE: 11/14/2001

TIME: 15:36:21

Input Set : N:\Crf3\RULE60\09757982A.txt

Output Set: N:\CRF3\11142001\I757982A.raw

3 <110> APPLICANT: Acton, Susan  
 5 <120> TITLE OF INVENTION: NOVEL PROTEIN KINASE MOLECULES AND USES THEREFOR  
 7 <130> FILE REFERENCE: MNI-050  
 C--> 9 <140> CURRENT APPLICATION NUMBER: US/09/757,982A  
 10 <141> CURRENT FILING DATE: 2001-01-10  
 12 <150> PRIOR APPLICATION NUMBER: 09/163,115  
 13 <151> PRIOR FILING DATE: 1998-09-29  
 15 <160> NUMBER OF SEQ ID NOS: 15  
 17 <170> SOFTWARE: PatentIn Ver. 2.0  
 19 <210> SEQ ID NO: 1  
 20 <211> LENGTH: 4137  
 21 <212> TYPE: DNA  
 22 <213> ORGANISM: Homo sapiens  
 24 <220> FEATURE:  
 25 <223> OTHER INFORMATION: 'n' at positions 2872, 3597 and 3682 may be any nucleic acid  
 27 <220> FEATURE:  
 28 <221> NAME/KEY: CDS  
 29 <222> LOCATION: (297)..(1202)  
 31 <400> SEQUENCE: 1  
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 34 actccggacg cgcctcgcag tgcgcagggt ggggtgccccg cgcctgcagc gtccgccggg 120  
 36 gcggcgccgc gggaggtggc cgacaggctc cgggcctcgc agcctcagcc cccggcccag 180  
 38 cgcgctttcc gacggcggcg ccgcgccgag ccacccgccc gcccaaggtc tctcgcgggc 240  
 40 gggagaacgg aaaactcca acttcttgag ttctaaagtt cctgttgctt cagaca atg 299  
 41 Met  
 42 1  
 44 gat gag caa tca caa gga atg caa ggg cca cct gtt cct cag ttc caa 347  
 45 Asp Glu Gln Ser Gln Gly Met Gln Gly Pro Pro Val Pro Gln Phe Gln  
 46 5 10 15  
 48 cca cag aag gcc tta cga ccg gat atg ggc tat aat aca tta gcc aac 395  
 49 Pro Gln Lys Ala Leu Arg Pro Asp Met Gly Tyr Asn Thr Leu Ala Asn  
 50 20 25 30  
 52 ttt cga ata gaa aag aaa att ggt cgc gga caa ttt agt gaa gtt tat 443  
 53 Phe Arg Ile Glu Lys Lys Ile Gly Arg Gly Gln Phe Ser Glu Val Tyr  
 54 35 40 45  
 56 aga gca gcc tgt ctc ttg gat gga gta cca gta gct tta aaa aaa gtg 491  
 57 Arg Ala Ala Cys Leu Leu Asp Gly Val Pro Val Ala Leu Lys Lys Val  
 58 50 55 60 65  
 60 cag ata ttt gat tta atg gat gcc aaa gca cgt gct gat tgc atc aaa 539  
 61 Gln Ile Phe Asp Leu Met Asp Ala Lys Ala Arg Ala Asp Cys Ile Lys  
 62 70 75 80  
 64 gaa ata gat ctt ctt aag caa ctc aac cat cca aat gta ata aaa tat 587  
 65 Glu Ile Asp Leu Leu Lys Gln Leu Asn His Pro Asn Val Ile Lys Tyr  
 66 85 90 95  
 68 tat gca tca ttc att gaa gat aat gaa cta aac ata gtt ttg gaa cta 635  
 69 Tyr Ala Ser Phe Ile Glu Asp Asn Glu Leu Asn Ile Val Leu Glu Leu  
 70 100 105 110

ENTERED

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72 gca gat gct ggc gac cta tcc aga atg atc aag cat ttt aag aag caa 683
73 Ala Asp Ala Gly Asp Leu Ser Arg Met Ile Lys His Phe Lys Lys Gln
74 115 120 125
76 aag agg cta att cct gaa aga act gtt tgg aag tat ttt gtt cag ctt 731
77 Lys Arg Leu Ile Pro Glu Arg Thr Val Trp Lys Tyr Phe Val Gln Leu
78 130 135 140 145
80 tgc agt gca ttg gaa cac atg cat tct cga aga gtc atg cat aga gat 779
81 Cys Ser Ala Leu Glu His Met His Ser Arg Arg Val Met His Arg Asp
82 150 155 160
84 ata aaa cca gct aat gtg ttc att aca gcc act ggg gtg gta aaa ctt 827
85 Ile Lys Pro Ala Asn Val Phe Ile Thr Ala Thr Gly Val Val Lys Leu
86 165 170 175
88 gga gat ctt ggg ctt ggc cgg ttt ttc agc tca aaa acc aca gct gca 875
89 Gly Asp Leu Gly Leu Gly Arg Phe Phe Ser Ser Lys Thr Thr Ala Ala
90 180 185 190
92 cat tct tta gtt ggt acg cct tat tac atg tct cca gag aga ata cat 923
93 His Ser Leu Val Gly Thr Pro Tyr Tyr Met Ser Pro Glu Arg Ile His
94 195 200 205
96 gaa aat gga tac aac ttc aaa tct gac atc tgg tct ctt ggc tgt cta 971
97 Glu Asn Gly Tyr Asn Phe Lys Ser Asp Ile Trp Ser Leu Gly Cys Leu
98 210 215 220 225
100 cta tat gag atg gct gca tta caa agt cct ttc tat ggt gac aaa atg 1019
101 Leu Tyr Glu Met Ala Ala Leu Gln Ser Pro Phe Tyr Gly Asp Lys Met
102 230 235 240
104 aat tta tac tca ctg tgt aag aag ata gaa cag tgt gac tac cca cct 1067
105 Asn Leu Tyr Ser Leu Cys Lys Lys Ile Glu Gln Cys Asp Tyr Pro Pro
106 245 250 255
108 ctt cct tca gat cac tat tca gaa gaa ctc cga cag tta gtt aat atg 1115
109 Leu Pro Ser Asp His Tyr Ser Glu Glu Leu Arg Gln Leu Val Asn Met
110 260 265 270
112 tgc atc aac cca gat cca gag aag cga cca gac gtc acc tat gtt tat 1163
113 Cys Ile Asn Pro Asp Pro Glu Lys Arg Pro Asp Val Thr Tyr Val Tyr
114 275 280 285
116 gac gta gca aag agg atg cat gca tgc act gca agc agc taaacatgca 1212
117 Asp Val Ala Lys Arg Met His Ala Cys Thr Ala Ser Ser
118 290 295 300
120 agatcatgaa gagtgtaacc aaagtaattg aaagtatttt gtgcaaagtc gtacctscce 1272
122 atttatgtct ggggtgtaag attaataattt cagagctagt gtgctctgaa tccttaacca 1332
124 gttttcatat aagcttcatt ttgtaccagt cacctaaatc acctccttgc aacccccaaa 1392
126 tgactttgga ataactgaat tgcattgtag gagagaaaat gaaacatgat ggttttgaat 1452
128 ggctaaagggt ttatagaatt tcttacagtt ttctgctgat aaattgtgtt tagatagact 1512
130 gtcagtgcc aatattgaag gtgcagcttg gcacacatca gaatagactc atacctgaga 1572
132 aaaagtatct gaacatgtga cttgtttctt ttttagtaat ttatggacat tgagatgaac 1632
134 acaattgtga acttttgtga agattttatt tttaaacgtt tgaagtacta gtttttagttc 1692
136 ttagcagagt agttttcaaa tatgattctt atgataaatg tagacacaaa ctatttgaga 1752
138 aacattttaga actcttagct tatacattca aaatgtaact attaaatgtg aagatttgagg 1812
140 gacaaaatgt gagtcagaca ctgaagagtt ttttgttttg ttttaatat tttgatattc 1872
142 tctttgcatt gaaatggtat aaatgaatcc atttaaaaag tgggttaagga tttgttttagc 1932
144 tgggtgtgata ataattttta aagttgcaca ttgccaagg ctttttttgt gtgtttttat 1992

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146 tgttggtttgt acatttgaaa aatattcttt gaataacctt gcagtactat atttcaagrt 2052
148 ttctttataa atttaagtgc attttaactc ataattgtac actataatat aagcctaagt 2112
150 ttttattcat aagttttatt gaagttctga tcggtcccct tcagaaattt ttttatatta 2172
152 ttcttcaagt tactttctta tttatattgt atgtgcattt tatccattaa tgtttcatac 2232
154 tttctgagag tataataccc ttttaaaaga tatttggtat accaataactt ttcctggatt 2292
156 gaaaactttt tttaaacttt ttaaaatttg ggccactctg tatgcatatg tttggtcttg 2352
158 ttaaagagga agaaaggatg tgtgtttatac tgtacctgtg aatgttgata cagttacaat 2412
160 ttatttgaca aggttgtaat tctagaatat gcttaataaa atgaaaactg gccatgacta 2472
162 cagccagaac tgttatgaga ttaacatttc tattgagaag cttttgagta aagtactgta 2532
164 tttgttcatg aagatgactg agatggtaac acttcgtgta gcttaaggaa atgggcagaa 2592
166 tttcgtaaat gctgttggtc agatgtgttt tccctgaatg ctttcgtatt agtggcgacc 2652
168 agtttctcac agaattgtga agcctgaagg ccaagaggaa gtcactgtta aaggactctg 2712
170 tgccatctta caaccttgga tgaattatcc tgccaacgtg aaaacctcat gttcaaagaa 2772
172 cacttccctt tagccgatgt aactgctggt tttgtttttc atatgtgttt ttcttacact 2832
W--> 174 catttgaatg ctttcaagca tttgtaaact taaaaaaan wawaaagggc aaaaagtctg 2892
176 aaccttggtt ttctgaaatc taatcagtta tgtatgggtt ctgaagggta attttatatt 2952
178 ggaataggta aagcgaaacc tgttttgtcw tgtttttctt gagggctaga tgcatttttt 3012
180 ttctcacact cttaatgact tttaacattt atactgagca tccatagata tattcctaga 3072
182 agtatgagaa gaattattct tattgaccat taatgtcatg ttcattttta tgtaataata 3132
184 ttgagatgaa atgttctctg gttggaacag atactctctt ttttttctt gcaatcttta 3192
186 agaatacata gatctaaaat tcattagctt gacctctcaa agtaactttt aagtaaagat 3252
188 taaagctttt cttctcagtg aatatatctg ctagaaggaa atagctggga agaatttaat 3312
190 gatcagggaa attcattatt tctatatgtg gaaacttttt gcttcgaata ttgtatcttt 3372
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196 acctataaaa tgttctttat atgtgttcat aagtaaattt tatattgatt aagttaaact 3552
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200 acattggkac cagttaccca ggtgaaaata kggagtaact ttgttttgta tggtaagggt 3672
W--> 202 taggaatggn ggatgaaggg tatctctata taaataaagt gctcaacaat gtgcaatgat 3732
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208 gatatttatt ttaaccaaaa tgttactcac attaaatgtt tattctttta aatgaatgta 3912
210 ttatgttttt aaccacaaaa tgcatactta ccctgtgcct catatttcaa tagtactgta 3972
212 atatggacat cttttgtgaa atacttttat tttgttatgc tttaaatata catacaaaaa 4032
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220 <211> LENGTH: 302
221 <212> TYPE: PRT
222 <213> ORGANISM: Homo sapiens
224 <400> SEQUENCE: 2
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226 1 5 10 15
228 Gln Pro Gln Lys Ala Leu Arg Pro Asp Met Gly Tyr Asn Thr Leu Ala
229 20 25 30
231 Asn Phe Arg Ile Glu Lys Lys Ile Gly Arg Gly Gln Phe Ser Glu Val
232 35 40 45
234 Tyr Arg Ala Ala Cys Leu Leu Asp Gly Val Pro Val Ala Leu Lys Lys
235 50 55 60

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237 Val Gln Ile Phe Asp Leu Met Asp Ala Lys Ala Arg Ala Asp Cys Ile
238 65 70 75 80
240 Lys Glu Ile Asp Leu Leu Lys Gln Leu Asn His Pro Asn Val Ile Lys
241 85 90 95
243 Tyr Tyr Ala Ser Phe Ile Glu Asp Asn Glu Leu Asn Ile Val Leu Glu
244 100 105 110
246 Leu Ala Asp Ala Gly Asp Leu Ser Arg Met Ile Lys His Phe Lys Lys
247 115 120 125
249 Gln Lys Arg Leu Ile Pro Glu Arg Thr Val Trp Lys Tyr Phe Val Gln
250 130 135 140
252 Leu Cys Ser Ala Leu Glu His Met His Ser Arg Arg Val Met His Arg
253 145 150 155 160
255 Asp Ile Lys Pro Ala Asn Val Phe Ile Thr Ala Thr Gly Val Val Lys
256 165 170 175
258 Leu Gly Asp Leu Gly Leu Gly Arg Phe Phe Ser Ser Lys Thr Thr Ala
259 180 185 190
261 Ala His Ser Leu Val Gly Thr Pro Tyr Tyr Met Ser Pro Glu Arg Ile
262 195 200 205
264 His Glu Asn Gly Tyr Asn Phe Lys Ser Asp Ile Trp Ser Leu Gly Cys
265 210 215 220
267 Leu Leu Tyr Glu Met Ala Ala Leu Gln Ser Pro Phe Tyr Gly Asp Lys
268 225 230 235 240
270 Met Asn Leu Tyr Ser Leu Cys Lys Lys Ile Glu Gln Cys Asp Tyr Pro
271 245 250 255
273 Pro Leu Pro Ser Asp His Tyr Ser Glu Glu Leu Arg Gln Leu Val Asn
274 260 265 270
276 Met Cys Ile Asn Pro Asp Pro Glu Lys Arg Pro Asp Val Thr Tyr Val
277 275 280 285
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280 290 295 300
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286 <213> ORGANISM: Homo sapiens
288 <220> FEATURE:
289 <221> NAME/KEY: CDS
290 <222> LOCATION: (1)..(906)
292 <400> SEQUENCE: 3
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294 Met Asp Glu Gln Ser Gln Gly Met Gln Gly Pro Pro Val Pro Gln Phe
295 1 5 10 15
297 caa cca cag aag gcc tta cga ccg gat atg ggc tat aat aca tta gcc 96
298 Gln Pro Gln Lys Ala Leu Arg Pro Asp Met Gly Tyr Asn Thr Leu Ala
299 20 25 30
301 aac ttt cga ata gaa aag aaa att ggt cgc gga caa ttt agt gaa gtt 144
302 Asn Phe Arg Ile Glu Lys Lys Ile Gly Arg Gly Gln Phe Ser Glu Val
303 35 40 45
305 tat aga gca gcc tgt ctc ttg gat gga gta cca gta gct tta aaa aaa 192
306 Tyr Arg Ala Ala Cys Leu Leu Asp Gly Val Pro Val Ala Leu Lys Lys

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307      50      55      60
309 gtg cag ata ttt gat tta atg gat gcc aaa gca cgt gct gat tgc atc 240
310 Val Gln Ile Phe Asp Leu Met Asp Ala Lys Ala Arg Ala Asp Cys Ile
311 65      70      75      80
313 aaa gaa ata gat ctt ctt aag caa ctc aac cat cca aat gta ata aaa 288
314 Lys Glu Ile Asp Leu Leu Lys Gln Leu Asn His Pro Asn Val Ile Lys
315      85      90      95
317 tat tat gca tca ttc att gaa gat aat gaa cta aac ata gtt ttg gaa 336
318 Tyr Tyr Ala Ser Phe Ile Glu Asp Asn Glu Leu Asn Ile Val Leu Glu
319      100      105      110
321 cta gca gat gct ggc gac cta tcc aga atg atc aag cat ttt aag aag 384
322 Leu Ala Asp Ala Gly Asp Leu Ser Arg Met Ile Lys His Phe Lys Lys
323      115      120      125
325 caa aag agg cta att cct gaa aga act gtt tgg aag tat ttt gtt cag 432
326 Gln Lys Arg Leu Ile Pro Glu Arg Thr Val Trp Lys Tyr Phe Val Gln
327      130      135      140
329 ctt tgc agt gca ttg gaa cac atg cat tct cga aga gtc atg cat aga 480
330 Leu Cys Ser Ala Leu Glu His Met His Ser Arg Arg Val Met His Arg
331 145      150      155      160
333 gat ata aaa cca gct aat gtg ttc att aca gcc act ggg gtg gta aaa 528
334 Asp Ile Lys Pro Ala Asn Val Phe Ile Thr Ala Thr Gly Val Val Lys
335      165      170      175
337 ctt gga gat ctt ggg ctt ggc cgg ttt ttc agc tca aaa acc aca gct 576
338 Leu Gly Asp Leu Gly Leu Gly Arg Phe Phe Ser Ser Lys Thr Thr Ala
339      180      185      190
341 gca cat tct tta gtt ggt acg cct tat tac atg tct cca gag aga ata 624
342 Ala His Ser Leu Val Gly Thr Pro Tyr Tyr Met Ser Pro Glu Arg Ile
343      195      200      205
345 cat gaa aat gga tac aac ttc aaa tct gac atc tgg tct ctt ggc tgt 672
346 His Glu Asn Gly Tyr Asn Phe Lys Ser Asp Ile Trp Ser Leu Gly Cys
347      210      215      220
349 cta cta tat gag atg gct gca tta caa agt cct ttc tat ggt gac aaa 720
350 Leu Leu Tyr Glu Met Ala Ala Leu Gln Ser Pro Phe Tyr Gly Asp Lys
351 225      230      235      240
353 atg aat tta tac tca ctg tgt aag aag ata gaa cag tgt gac tac cca 768
354 Met Asn Leu Tyr Ser Leu Cys Lys Lys Ile Glu Gln Cys Asp Tyr Pro
355      245      250      255
357 cct ctt cct tca gat cac tat tca gaa gaa ctc cga cag tta gtt aat 816
358 Pro Leu Pro Ser Asp His Tyr Ser Glu Glu Leu Arg Gln Leu Val Asn
359      260      265      270
361 atg tgc atc aac cca gat cca gag aag cga cca gac gtc acc tat gtt 864
362 Met Cys Ile Asn Pro Asp Pro Glu Lys Arg Pro Asp Val Thr Tyr Val
363      275      280      285
365 tat gac gta gca aag agg atg cat gca tgc act gca agc agc 906
366 Tyr Asp Val Ala Lys Arg Met His Ala Cys Thr Ala Ser Ser
367      290      295      300
370 <210> SEQ ID NO: 4
371 <211> LENGTH: 2120
372 <212> TYPE: DNA

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L:9 M:270 C: Current Application Number differs, Replaced Current Application Number  
L:174 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1  
L:198 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1  
L:202 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1